**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

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| In re Patent Application of: | Group Art Unit: 1634 |
| CUNNINGHAM *et al.* | Examiner: Goldberg, J. |
| Serial No. 09/954,586 | Atty. Docket No. GP116-03.UT |
| Filed: September 11, 2001 | Confirmation No. 7245 |
| For: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF CRYPTOSPORIDIUM PARVUM ORGANISMS IN A TEST SAMPLE | |

**RESPONSE TO RESTRICTION REQUIREMENT & AMENDMENT**

Commissioner for Patents
Washington, D.C. 20231

Sir:

In response to the Examiner's Office Action mailed on November 22, 2002, in the above-captioned application, Applicants have amended the claims herein to recite a single group of related probe target sequences (SEQ ID Nos. 6, 10, 14 and 18), a single group of related helper oligonucleotide target sequences (SEQ ID Nos. 29, 33, 37 and 41), and a single group of related amplification primer target sequences (SEQ. ID. Nos. 48, 54, 60 and 66) in the independent claims. Each group of related sequences includes a base DNA sequence, the DNA complement of the base sequence, and the RNA equivalents of the base sequence and its complement.

**IN THE CLAIMS:**

Please cancel claims 2-5, 24-28, 30-36, 41-49, 54-58, 61-83, 85 and 86 without prejudice.

Kindly substitute and add the following claims:

1. (Amended) A hybridization assay probe comprising an oligonucleotide which hybridizes to a target sequence present in nucleic acid derived from a *Cryptosporidium parvum* organism in a test sample under stringent conditions to form a probe:target hybrid stable for detection, said oligonucleotide having an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in the target sequence, wherein the target sequence is selected from the group consisting of SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14 and SEQ ID NO:18, and wherein said probe does not hybridize to nucleic acid derived from a *Cryptosporidium muris*, *Cryptosporidium baileyi* or *Crptosporidium wrairi* organism in the test sample to form a probe:non-target hybrid stable for detection under the stringent conditions.

20. (Amended) A hybridization assay probe comprising an oligonucleotide which hybridizes to a target sequence present in nucleic acid derived from a *Cryptosporidium parvum* organism in a test sample under stringent conditions to form a probe:target hybrid stable for detection, said oligonucleotide having a base sequence which is at least 80% complementary to the base sequence of the target sequence, wherein the target sequence has a base sequence selected from the group consisting of SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14 and SEQ ID NO:18, and wherein said probe does not hybridize to nucleic acid derived from a *Cryptosporidium muris*, *Cryptosporidium baileyi* or *Crptosporidium wrairi* organism in the test sample to form a probe:non-target hybrid stable for detection under the stringent conditions.

21. (Amended) An oligonucleotide probe which hybridizes to a target sequence present in nucleic acid derived from a *Cryptosporidium parvum* organism in a test sample under stringent conditions to form a probe:target hybrid stable for detection, wherein the base sequence of said probe is at least 80% complementary to the base sequence of the target sequence, wherein the target sequence is selected from the group consisting of SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14 and SEQ ID NO:18, and wherein said probe does not hybridize to nucleic acid derived from

a *Cryptosporidium muris*, *Cryptosporidium baileyi* or *Crptosporidium wrairi* organism in the test sample to form a probe:non-target hybrid stable for detection under the stringent conditions.

22. (Amended) An oligonucleotide probe which hybridizes to a target sequence present in nucleic acid derived from a *Cryptosporidium parvum* organism in a test sample under stringent conditions to form a probe:target hybrid stable for detection, wherein the base sequence of said probe is fully complementary to the base sequence of the target sequence, wherein the target sequence is selected from the group consisting of SEQ ID NO:6 SEQ ID NO:10, SEQ ID NO:14 and SEQ ID NO:18, and wherein said probe does not hybridize to nucleic acid derived from a *Cryptosporidium muris*, *Cryptosporidium baileyi* or *Crptosporidium wrairi* organism in the test sample to form a probe:non-target hybrid stable for detection under the stringent conditions.

23. (Amended) A probe mix comprising the probe of claim 1 and a first helper oligonucleotide having an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in a target sequence selected from the group consisting of SEQ ID NO:29, SEQ ID NO:33, SEQ ID NO:37 and SEQ ID NO:41.

29. (Amended) The probe mix of claim 23 further comprising a second helper oligonucleotide having an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in a target sequence selected from the group consisting of SEQ ID NO:32, SEQ ID NO:36, SEQ ID NO:40 and SEQ ID NO:44.

38. (Amended) The method of claim 37 further comprising providing to the test sample a first amplification primer under amplification conditions, said first primer comprising an oligonucleotide having an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in a target sequence selected from the group

consisting of SEQ ID NO:48, SEQ ID NO:54, SEQ ID NO:60 and SEQ ID NO:66, and wherein said primer optionally includes a 5' sequence which is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

39. (Amended) The method of claim 38 further comprising providing to the test sample a second amplification primer comprising an oligonucleotide having an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in a target sequence selected from the group consisting of SEQ ID NO:45, SEQ ID NO:51, SEQ ID NO:57 and SEQ ID NO:63.

40. (Amended) The method of claim 38 further comprising providing to the test sample a second amplification primer comprising an oligonucleotide having an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in a target sequence selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64.

53. (Amended) A kit comprising, in packaged combination, first and second oligonucleotides for use in determining the presence of a *Cryptosporidium parvum* organism in a test sample, each of said oligonucleotides having an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in a target sequence contained in nucleic acid derived from a *Cryptosporidium parvum* organism, wherein:

the target sequence of said first oligonucleotide is selected from the group consisting of SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14 and SEQ ID NO:18;

the target sequence of said second oligonucleotide is selected from the group consisting of SEQ ID NO:48, SEQ ID NO:54, SEQ ID NO:60 and SEQ ID NO:66; and

said second oligonucleotide optionally includes a 5' sequence which is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

59. (Amended) The kit of claim 53 further comprising a third oligonucleotide, wherein said third oligonucleotide has an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in a target sequence contained in nucleic acid derived from a *Cryptosporidium* organism, and wherein the target sequence of said third oligonucleotide is selected from the group consisting of SEQ ID NO:45, SEQ ID NO:51, SEQ ID NO:57 and SEQ ID NO:63.

60. (Amended) The kit of claim 53 further comprising a third oligonucleotide, wherein said third oligonucleotide has an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in a target sequence contained in nucleic acid derived from a *Cryptosporidium* organism, and wherein the target sequence of said third oligonucleotide is selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64.

84. (Amended) A kit comprising, in packaged combination, first and second oligonucleotides for use in determining the presence of a *Cryptosporidium parvum* organism in a test sample, each of said oligonucleotides having an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in a target sequence contained in nucleic acid derived from a *Cryptosporidium parvum* organism, wherein:

the target sequence of said first oligonucleotide is selected from the group consisting of SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14 and SEQ ID NO:18; and

the target sequence of said second oligonucleotide is selected from the group consisting of SEQ ID NO:29, SEQ ID NO:33, SEQ ID NO:37 and SEQ ID NO:41.

87. (New) The probe of claim 1, wherein the base sequence of said probe comprises the base sequence of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 or SEQ ID NO:17.

88. (New) The probe of claim 1, wherein the base sequence of said probe consists of or is contained within the base sequence of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 or SEQ ID NO:17.

89. (New) The probe of claim 1, wherein the base sequence of said probe consists of the base sequence of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 or SEQ ID NO:17.

90. (New) The probe of claim 1, wherein the base sequence of said probe comprises the base sequence of SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15 or SEQ ID NO:19.

91. (New) The probe of claim 1, wherein the base sequence of said probe consists of or is contained within the base sequence of SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15 or SEQ ID NO:19.

92. (New) The probe of claim 1, wherein the base sequence of said probe consists of the base sequence of SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15 or SEQ ID NO:19.

93. (New) The probe of claim 20, wherein said oligonucleotide has a base sequence which is 100% complementary to the base sequence of the target sequence.

94. (New) A probe mix comprising the probe of claim 20 and a first helper oligonucleotide having a base sequence which is at least 80% complementary to the base sequence

of a target sequence selected from the group consisting of SEQ ID NO:29, SEQ ID NO:33, SEQ ID NO:37 and SEQ ID NO:41.

95. (New) The probe mix of claim 94 further comprising a second helper oligonucleotide having a base sequence which is at least 80% complementary to the base sequence of a target sequence selected from the group consisting of SEQ ID NO:32, SEQ ID NO:36, SEQ ID NO:40 and SEQ ID NO:44.

96. (New) A probe mix comprising the probe of claim 21 and a first helper oligonucleotide, wherein the base sequence of said first helper oligonucleotide is at least 80% complementary to the base sequence of a target sequence selected from the group consisting of SEQ ID NO:29, SEQ ID NO:33, SEQ ID NO:37 and SEQ ID NO:41.

97. (New) The probe mix of claim 96 further comprising a second helper oligonucleotide, wherein the base sequence of said second helper oligonucleotide is at least 80% complementary to the base sequence of a target sequence selected from the group consisting of SEQ ID NO:32, SEQ ID NO:36, SEQ ID NO:40 and SEQ ID NO:44.

98. (New) A probe mix comprising the probe of claim 22 and a first helper oligonucleotide, wherein the base sequence of said first helper oligonucleotide is fully complementary to the base sequence of a target sequence selected from the group consisting of SEQ ID NO:29, SEQ ID NO:33, SEQ ID NO:37 and SEQ ID NO:41.

99. (New) The probe mix of claim 98 further comprising a second helper oligonucleotide, wherein the base sequence of said second helper oligonucleotide is fully complementary to the base sequence of a target sequence selected from the group consisting of SEQ ID NO:32, SEQ ID NO:36, SEQ ID NO:40 and SEQ ID NO:44.

100. (New) The probe mix of claim 23, wherein the base sequence of said probe comprises the base sequence of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 or SEQ ID NO:17.

101. (New) The probe mix of claim 23, wherein the base sequence of said probe consists of or is contained within the base sequence of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 or SEQ ID NO:17.

102. (New) The probe mix of claim 23, wherein the base sequence of said probe consists of the base sequence of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 or SEQ ID NO:17.

103. (New) The probe mix of claim 23, wherein the base sequence of said probe comprises the base sequence of SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15 or SEQ ID NO:19.

104. (New) The probe mix of claim 23, wherein the base sequence of said probe consists of or is contained within the base sequence of SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15 or SEQ ID NO:19.

105. (New) The probe mix of claim 23, wherein the base sequence of said probe consists of the base sequence of SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15 or SEQ ID NO:19.

106. (New) A probe mix comprising the probe of claim 93 and a first helper oligonucleotide having a base sequence which is 100% complementary to the base sequence of a target sequence selected from the group consisting of SEQ ID NO:29, SEQ ID NO:33, SEQ ID NO:37 and SEQ ID NO:41.

107. (New) The probe mix of claim 106 further comprising a second helper oligonucleotide having a base sequence which is 100% complementary to the base sequence of a target sequence selected from the group consisting of SEQ ID NO:32, SEQ ID NO:36, SEQ ID NO:40 and SEQ ID NO:44.

108. (New) The method of claim 37, wherein the base sequence of said probe comprises the base sequence of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 or SEQ ID NO:17.

109. (New) The method of claim 37, wherein the base sequence of said probe consists of or is contained within the base sequence of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 or SEQ ID NO:17.

110. (New) The method of claim 37, wherein the base sequence of said probe consists of the base sequence of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 or SEQ ID NO:17.

111. (New) The method of claim 37, wherein the base sequence of said probe comprises the base sequence of SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15 or SEQ ID NO:19.

112. (New) The method of claim 37, wherein the base sequence of said probe consists of or is contained within the base sequence of SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15 or SEQ ID NO:19.

113. (New) The method of claim 37, wherein the base sequence of said probe consists of the base sequence of SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15 or SEQ ID NO:19.

114. (New) The method of claim 50 further comprising providing to the test sample a first amplification primer under amplification conditions, said first primer comprising an oligonucleotide having a base sequence which is at least 80% complementary to a base sequence selected from the group consisting of SEQ ID NO:48, SEQ ID NO:54, SEQ ID NO:60 and SEQ ID NO:66, and wherein said primer optionally includes a 5' sequence which is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

115. (New) The method of claim 114 further comprising providing to the test sample a second amplification primer comprising an oligonucleotide having a base sequence which is at least 80% complementary to a base sequence selected from the group consisting of SEQ ID NO:45, SEQ ID NO:51, SEQ ID NO:57 and SEQ ID NO:63.

116. (New) The method of claim 114 further comprising providing to the test sample a second amplification primer comprising an oligonucleotide having a base sequence which is at least 80% complementary to a base sequence selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64.

117. (New) The method of claim 50, wherein said oligonucleotide has a base sequence which is 100% complementary to the base sequence of the target sequence.

118. (New) The method of claim 117 further comprising providing to the test sample a first amplification primer under amplification conditions, said first primer comprising an oligonucleotide having a base sequence which is 100% complementary to a base sequence selected

from the group consisting of SEQ ID NO:48, SEQ ID NO:54, SEQ ID NO:60 and SEQ ID NO:66, and wherein said primer optionally includes a 5' sequence which is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

119. (New) The method of claim 118 further comprising providing to the test sample a second amplification primer comprising an oligonucleotide having a base sequence which is 100% complementary to a base sequence selected from the group consisting of SEQ ID NO:45, SEQ ID NO:51, SEQ ID NO:57 and SEQ ID NO:63.

120. (New) The method of claim 118 further comprising providing to the test sample a second amplification primer comprising an oligonucleotide having a base sequence which is 100% complementary to a base sequence selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64.

121. (New) The method of claim 51 further comprising providing to the test sample a first amplification primer under amplification conditions, wherein the base sequence of said first primer is at least 80% complementary to a base sequence selected from the group consisting of SEQ ID NO:48, SEQ ID NO:54, SEQ ID NO:60 and SEQ ID NO:66, and wherein said primer optionally includes a 5' sequence which is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

122. (New) The method of claim 121 further comprising providing to the test sample a second amplification primer, wherein the base sequence of said second primer is at least 80% complementary to a base sequence selected from the group consisting of SEQ ID NO:45, SEQ ID NO:51, SEQ ID NO:57 and SEQ ID NO:63.

123. (New) The method of claim 121 further comprising providing to the test sample a second amplification primer, wherein the base sequence of said second primer is at least 80% complementary to a base sequence selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64.

124. (New) The method of claim 52 further comprising providing to the test sample a first amplification primer under amplification conditions, wherein the base sequence of said first primer is fully complementary to a base sequence selected from the group consisting of SEQ ID NO:48, SEQ ID NO:54, SEQ ID NO:60 and SEQ ID NO:66, and wherein said primer optionally includes a 5' sequence which is recognized by an RNA polymerase or which enhances initiation or elongation by an RNA polymerase.

125. (New) The method of claim 124 further comprising providing to the test sample a second amplification primer, wherein the base sequence of said second primer is fully complementary to a base sequence selected from the group consisting of SEQ ID NO:45, SEQ ID NO:51, SEQ ID NO:57 and SEQ ID NO:63.

126. (New) The method of claim 124 further comprising providing to the test sample a second amplification primer, wherein the base sequence of said second primer is fully complementary to a base sequence selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64.

127. (New) The kit of claim 53, wherein the base sequence of said first oligonucleotide comprises the base sequence of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 or SEQ ID NO:17.

128. (New) The kit of claim 53, wherein the base sequence of said first oligonucleotide consists of or is contained within the base sequence of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 or SEQ ID NO:17.

129. (New) The kit of claim 53, wherein the base sequence of said first oligonucleotide consists of the base sequence of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 or SEQ ID NO:17.

130. (New) The kit of claim 53, wherein the base sequence of said first oligonucleotide comprises the base sequence of SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15 or SEQ ID NO:19.

131. (New) The kit of claim 53, wherein the base sequence of said first oligonucleotide consists of or is contained within the base sequence of SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15 or SEQ ID NO:19.

132. (New) The kit of claim 53, wherein the base sequence of said first oligonucleotide consists of the base sequence of SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15 or SEQ ID NO:19.

133. (New) The kit of claim 53, wherein each of said oligonucleotides has a base region which is at least 80% complementary to the base sequence of the target sequence.

134. (New) The kit of claim 53, wherein each of said oligonucleotides has a base region which is 100% complementary to the base sequence of the target sequence.

135. (New) The kit of claim 53, wherein the base sequence of each of said oligonucleotides is at least 80% complementary to the base sequence of the target sequence.

136. (New) The kit of claim 53, wherein the base sequence of each of said oligonucleotides is fully complementary to the base sequence of the target sequence.

137. (New) The kit of claim 59, wherein each of said oligonucleotides has a base region which is at least 80% complementary to the base sequence of the target sequence.

138. (New) The kit of claim 59, wherein each of said oligonucleotides has a base region which is 100% complementary to the base sequence of the target sequence.

139. (New) The kit of claim 59, wherein the base sequence of each of said oligonucleotides is at least 80% complementary to the base sequence of the target sequence.

140. (New) The kit of claim 59, wherein the base sequence of each of said oligonucleotides is fully complementary to the base sequence of the target sequence.

141. (New) The kit of claim 60, wherein each of said oligonucleotides has a base region which is at least 80% complementary to the base sequence of the target sequence.

142. (New) The kit of claim 60, wherein each of said oligonucleotides has a base region which is 100% complementary to the base sequence of the target sequence.

143. (New) The kit of claim 60, wherein the base sequence of each of said oligonucleotides is at least 80% complementary to the base sequence of the target sequence.

144. (New) The kit of claim 60, wherein the base sequence of each of said oligonucleotides is fully complementary to the base sequence of the target sequence.

145. (New) The kit of claim 84, wherein the base sequence of said first oligonucleotide comprises the base sequence of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 or SEQ ID NO:17.

146. (New) The kit of claim 84, wherein the base sequence of said first oligonucleotide consists of or is contained within the base sequence of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 or SEQ ID NO:17.

147. (New) The kit of claim 84, wherein the base sequence of said first oligonucleotide consists of the base sequence of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 or SEQ ID NO:17.

148. (New) The kit of claim 84, wherein the base sequence of said first oligonucleotide comprises the base sequence of SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15 or SEQ ID NO:19.

149. (New) The kit of claim 84, wherein the base sequence of said first oligonucleotide consists of or is contained within the base sequence of SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15 or SEQ ID NO:19.

150. (New) The kit of claim 84, wherein the base sequence of said first oligonucleotide consists of the base sequence of SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15 or SEQ ID NO:19.

151. (New) The kit of claim 84, wherein each of said oligonucleotides has a base region which is at least 80% complementary to the base sequence of the target sequence.

152. (New) The kit of claim 84, wherein each of said oligonucleotides has a base region which is 100% complementary to the base sequence of the target sequence.

153. (New) The kit of claim 84, wherein the base sequence of each of said oligonucleotides is at least 80% complementary to the base sequence of the target sequence.

154. (New) The kit of claim 84, wherein the base sequence of each of said oligonucleotides is fully complementary to the base sequence of the target sequence.

155. (New) The kit of claim 84 further comprising a third oligonucleotide, wherein said third oligonucleotide has an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in a target sequence contained in nucleic acid derived from a *Cryptosporidium parvum* organism, and wherein the target sequence of said third oligonucleotide is selected from the group consisting of SEQ ID NO:32, SEQ ID NO:36, SEQ ID NO:40 and SEQ ID NO:44.

156. (New) The kit of claim 155, wherein each of said oligonucleotides has a base region which is at least 80% complementary to the base sequence of the target sequence.

157. (New) The kit of claim 155, wherein each of said oligonucleotides has a base region which is 100% complementary to the base sequence of the target sequence.

158. (New) The kit of claim 155, wherein the base sequence of each of said oligonucleotides is at least 80% complementary to the base sequence of the target sequence.

159. (New) The kit of claim 155, wherein the base sequence of each of said oligonucleotides is fully complementary to the base sequence of the target sequence.

* * * * *

**Remarks**

Claims 1, 6-23, 29, 37-40, 50-53, 59, 60, 84 and 87-159 are presently pending in the subject application.

Claims 2-5, 24-28, 30-36, 41-49, 54-58, 61-83, 85 and 86 are canceled herein without prejudice to the prosecution of the subject matter of these claims in this or a future continuing application.

Claims 87-159 are newly added herein and find support in the specification and in the originally filed claims. No new matter is being added by the inclusion of these claims.

A marked-up version of the amendments is attached hereto in accordance with the provisions set forth in 37 C.F.R. § 1.121.

In response to the Examiner's Restriction Requirement, Applicants hereby elect the related target sequences of SEQ ID Nos. 6, 10, 14 and 18 as the basis for the claimed hybridization assay probes, the related target sequences of SEQ ID Nos. 29, 33, 37 and 41 as the basis for the helper olignucleotides claimed in combination with the elected hybridization assay probes, and the related target sequences of SEQ ID Nos. 48, 54, 60 and 66 as the basis for the amplification primers claimed in combination with the elected hybridization assay probes. The independent claims have

been amended in accordance with these elections. Amended and newly added dependent claims recite additional helper probes and amplification primers, as allowed by the Examiner during a telephone interview with Applicants' representative on or about December 12, 2002.

Applicants submit that the subject application is in condition for allowance and early Notice to that effect is earnestly solicited.

Please charge the excess claims fee due under 37 C.F.R. § 1.16(c), and any other fee which may be due, to Deposit Account No. 07-0835 in the name of Gen-Probe Incorporated.

**Certificate of Transmission**

I hereby certify that this correspondence (and any referred to as attached) is being sent by facsimile to 703-872-9306 on the date indicated below to the Commissioner for Patents, Washington, D.C. 20231.

Respectfully Submitted,

Date: December 19, 2002

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